

Asthma phenotyping using exhaled volatile organic compounds

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Background: Asthma is one of the most prevalent chronic disorder worldwide, affecting 235 million people. This represents a serious public health issue associated with high health costs, mainly due to diagnosis and treatment. A European study has estimated the total cost of asthma to 19.3 billion of euros per year. Asthma is characterized by an inflammation of the airways, involving several different underlying mechanisms. Current therapies, using inhaled corticosteroids, remain ineffective in a large proportion of patients. Therefore, the characterization of the different inflammation phenotypes (i.e. eosinophilic, neutrophilic, paucigranulocytic, mixed granulocytic asthma) is of great importance to provide an adjusted treatment to each patient.

Methods: In this study, volatile organic compounds from breath of 89 asthmatic patients covering a range of different asthma phenotypes were analyzed. Among them, 33 had eosinophilic, 17 neutrophilic, 37 paucigranulocytic, and 2 mixed granulocytic asthma. The breath samples were collected into 5 L Tedlar® bags. Thermal desorption coupled with comprehensive two-dimensional gas chromatography – high resolution time-of-flight mass spectrometry was applied for the analysis. The data were split between training and test (60-40%). Several machine learning algorithms were used to investigate the ability of exhaled breath VOCs to distinguish between the inflammatory profiles.

Results: Random forest, support vector machine, decision trees and gradient boosting algorithms were used to select significant VOCs for asthma phenotyping and to build the classification model on the test set. ROC curve were constructed to evaluate the classification performance of the different models based on a test set using the selected VOCs in pair-classification scenarios.

Conclusions: Similar results were obtained for each machine learning algorithm and permitted the discrimination of patients according to their respective phenotypes. The present study supports the hypothesis that exhaled air analysis allows deeper understanding of asthma phenotypes and is going to lead to further development in clinical diagnosis.